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In re Application of

Application Number

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08-312,914

Sep. 30, 94

Paper No. _____

I hereby request access under 37 CFR 1.14(a)(1)(iv) to the application file record of the above-identified ABANDONED application, which is identified in, or to which a benefit is claimed, in the following document (as shown in the attachment):

United States Patent Application Publication No. 6,475,720, page, _____ line _____

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(12) **United States Patent**
Gray et al.



US006475720B1

(10) Patent No.: **US 6,475,720 B1**
(45) Date of Patent: **Nov. 5, 2002**

(54) **CHROMOSOME-SPECIFIC STAINING TO
DETECT GENETIC REARRANGEMENTS
ASSOCIATED WITH CHROMOSOME 3
AND/OR CHROMOSOME 17**

(75) Inventors: Joe W. Gray, Livmore, CA (US);
Daniel Pinkel, Walnut Creek, CA (US);
Olli-Pekka Kallioniemi, Tampere (FI);
Anne Kallioniemi, Tampere (FI);
Masaru Sakamoto, Tokyo (JP)

(73) Assignee: The Regents of the University of
California, Oakland, CA (US)

(*) Notice: Subject to any disclaimer, the term of this
patent is extended or adjusted under 35
U.S.C. 154(b) by 0 days.

(21) Appl. No.: 08/478,387

(22) Filed: Jun. 7, 1995

Related U.S. Application Data

(60) Division of application No. 08/312,914, filed on Sep. 30, 1994, now abandoned, which is a continuation of application No. 08/137,745, filed on Oct. 19, 1993, now abandoned, which is a continuation of application No. 08/015,390, filed on Feb. 8, 1993, now abandoned, which is a continuation of application No. 07/670,242, filed on Mar. 15, 1991, now abandoned, which is a continuation-in-part of application No. 07/659,974, filed on Feb. 22, 1991, now abandoned, which is a continuation-in-part of application No. 07/537,305, filed on Jun. 12, 1990, now abandoned, which is a continuation-in-part of application No. 07/497,098, filed on Mar. 20, 1990, now abandoned, which is a continuation of application No. 07/444,669, filed on Dec. 1, 1989, now abandoned, which is a continuation-in-part of application No. 06/957,793, filed on Dec. 4, 1986, now abandoned, which is a continuation-in-part of application No. 06/819,314, filed on Jan. 28, 1986, now abandoned.

(51) Int. Cl.⁷ C12Q 1/68; C07H 21/00

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536/24.3; 536/24.31

(58) Field of Search 435/6, 810; 436/501;
536/23.1, 24.1, 24.3-24.33, 25.3; 935/77.78

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Primary Examiner—Ardin H. Marschel

(74) Attorney, Agent, or Firm—Burns, Doane, Swecker &
Mathis, LLP

(57)

ABSTRACT

Methods and compositions for staining based upon nucleic acid sequences that employ nucleic acid probes are provided. Said methods produce staining patterns that can be tailored for specific cytogenetic analyses. Said probes are appropriate for in situ hybridization and stain both interphase and metaphase chromosomal material with reliable signals. The nucleic acid probes are typically of a complexity greater than 50 kb, the complexity depending upon the cytogenetic application. Methods and reagents are provided for the detection of genetic rearrangements. Probes and test kits are provided for use in detecting genetic rearrangements, particularly for use in tumor cytogenetics, in the detection of disease related loci, specifically cancer, such as chronic myelogenous leukemia (CML), retinoblastoma, ovarian and uterine cancers, and for biological dosimetry. Methods and reagents are described for cytogenetic research, for the differentiation of cytogenetically similar but genetically different diseases, and for many prognostic and diagnostic applications.

4 Claims, 22 Drawing Sheets



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